

SEQUENCE LISTING

<110> Basi, Guriq
Saldanha, Jose
Yednock, Ted

<120> Humanized Antibodies that Recognize
Beta-Amyloid Peptide

<130> ELN-002

<150> 60/251,892

<151> 2000-12-06

<160> 63

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 396

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)...(396)

<221> sig_peptide

<222> (1)...(60)

<400> 1

atg atg agt cct gcc cag ttc ctg ttt ctg tta gtg ctc tgg att cgg	48
Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg	
-20 -15 -10 -5	

gaa acc aac ggt tat gtt gtg atg acc cag act cca ctc act ttg tgg	96
Glu Thr Asn Gly Tyr Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser	
1 5 10	

gtt acc att gga caa cca gcc tcc atc tct tgc aag tca agt cag agc	144
Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser	
15 20 25	

ctc tta gat agt gat gga aag aca tat ttg aat tgg ttg tta cag agg	192
Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg	
30 35 40	

cca ggc cag tct cca aag cgc cta atc tat ctg gtg tct aaa ctg gac	240
Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp	
45 50 55 60	

tct gga gtc cct gac agg ttc act ggc agt gga tca ggg aca gat ttt	288
Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe	
65 70 75	

10010942-120604

```

aca ctg aaa atc agc aga ata gag gct gag gat ttg gga ctt tat tat 336
Thr Leu Lys Ile Ser Arg Ile Glu Ala Glu Asp Leu Gly Leu Tyr Tyr
      80                      85                      90

tgc tgg caa ggt aca cat ttt cct cgg acg ttc ggt gga ggc acc aag 384
Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys
      95                      100                      105

ctg gaa atc aaa 396
Leu Glu Ile Lys
      110

```

```

<210> 2
<211> 132
<212> PRT
<213> Mus musculus

```

```

<220>
<221> SIGNAL
<222> (1)...(20)

```

```

<400> 2
Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
-20                      -15                      -10                      -5
Glu Thr Asn Gly Tyr Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser
      1                      5                      10
Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
      15                      20                      25
Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg
      30                      35                      40
Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
45                      50                      55                      60
Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
      65                      70                      75
Thr Leu Lys Ile Ser Arg Ile Glu Ala Glu Asp Leu Gly Leu Tyr Tyr
      80                      85                      90
Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys
      95                      100                      105
Leu Glu Ile Lys
      110

```

```

<210> 3
<211> 414
<212> DNA
<213> Mus musculus

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<220>
<221> CDS
<222> (1)...(414)

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```

<221> sig_peptide
<222> (1)...(57)

```

100109412-120501

[illegible][illegible][illegible][illegible]

Glu	Trp	Val	Ala	Ser 50	Ile	Arg	Ser	Gly	Gly 55	Gly	Arg	Thr	Tyr	Tyr	Ser
Asp	Asn	Val	Lys 65	Gly	Arg	Phe	Thr	Ile 70	Ser	Arg	Glu	Asn	Ala 75	Lys	Asn
Thr	Leu	Tyr 80	Leu	Gln	Met	Ser	Ser 85	Leu	Lys	Ser	Glu	Asp 90	Thr	Ala	Leu
Tyr	Tyr 95	Cys	Val	Arg	Tyr	Asp 100	His	Tyr	Ser	Gly	Ser 105	Ser	Asp	Tyr	Trp
Gly 110	Gln	Gly	Thr	Thr	Ile 115	Thr	Val	Ser	Ser						

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<210> 5
<211> 132
<212> PRT
<213> Artificial Sequence
```

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<220>
<221> SIGNAL
<222> (1) ... (20)
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<223> humanized 3D6 light chain variable region

```
<400> 5
Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
-20              -15          -10                -5
Glu Thr Asn Gly Tyr Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro
             1               5            10
Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
      15                 20           25
Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Lys
    30         35       40
Pro Gly Gln Ser Pro Gln Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
45        50          55            60
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
      65                70          75
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
     80              85            90
Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gln Gly Thr Lys
   95              100          105
Val Glu Ile Lys
    110
```

```
<210> 6
<211> 125
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> SIGNAL
<222> (1) ... (19)
```

<400> 6

```

Met Gly Leu Leu Met Leu Trp Val Ser Gly Ser Ser Gly Asp Ile Val
      -15                      -10                      -5
Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala
      1                      5                      10
Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr
      15                      20                      25
Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu
      30                      35                      40                      45
Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe
      50                      55                      60
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
      65                      70                      75
Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Thr
      80                      85                      90
Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
      95                      100                      105

```

<210> 7
 <211> 100
 <212> PRT
 <213> Homo sapiens

```

<400> 7
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
      1                      5                      10                      15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
      20                      25                      30
Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
      35                      40                      45
Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
      50                      55                      60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
      65                      70                      75                      80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
      85                      90                      95
Leu Gln Thr Pro
      100

```

<210> 8
 <211> 138
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized 3D6 heavy chain variable region

<221> SIGNAL
 <222> (1)...(19)

```

<400> 8
Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
      -15                      -10                      -5
Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
      1                      5                      10

```

F09037-24607007

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 15 20 25
 Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 30 35 40 45
 Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser
 50 55 60
 Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
 65 70 75
 Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu
 80 85 90
 Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
 95 100 105
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 110 115

<210> 9
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 9
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Ala Val Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95
 Ala Lys Asp Asn Tyr Asp Phe Trp Ser Gly Thr Phe Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 10
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 10
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

10010942-120604

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys

<210> 11
 <211> 132
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> SIGNAL
 <222> (1)...(20)

<223> humanized 3D6 light chain variable region

<400> 11
 Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
 -20 -15 -10 -5
 Glu Thr Asn Gly Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro
 1 5 10
 Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
 15 20 25
 Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Lys
 30 35 40
 Pro Gly Gln Ser Pro Gln Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
 45 50 55 60
 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 65 70 75
 Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
 80 85 90
 Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gln Gly Thr Lys
 95 100 105
 Val Glu Ile Lys
 110

<210> 12
 <211> 138
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized 3D6 light chain variable region
 <221> SIGNAL
 <222> (1)...(19)

<400> 12
 Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
 -15 -10 -5
 Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
 1 5 10
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 15 20 25

FOOTNOTES

Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 30 35 40 45
 Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser
 50 55 60
 Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
 65 70 75
 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 80 85 90
 Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
 95 100 105
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 110 115

<210> 13
 <211> 393
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)...(393)
 <221> sig_peptide
 <222> (1)...(57)

<400> 13
 atg aag ttg cct gtt agg ctg ttg gta ctg atg ttc tgg att cct gct 48
 Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
 -15 -10 -5
 tcc agc agt gat gtt ttg atg acc caa act cca ctc tcc ctg cct gtc 96
 Ser Ser Ser Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val
 1 5 10
 agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag aac att 144
 Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Ile
 15 20 25
 ata cat agt aat gga aac acc tat tta gaa tgg tac ctg cag aaa cca 192
 Ile His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro
 30 35 40 45
 ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct 240
 Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
 50 55 60
 ggg gtc cca gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca 288
 Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 65 70 75
 ctc aag atc aag aaa gtg gag gct gag gat ctg gga att tat tac tgc 336
 Leu Lys Ile Lys Lys Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys
 80 85 90

10010942-120504


```

ttt caa ggt tca cat gtt ccg ctc acg ttc ggt gct ggg acc aag ctg 384
Phe Gln Gly Ser His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
    95                100                105

```

```

gag ctg gaa 393
Glu Leu Glu
110

```

```

<210> 14
<211> 131
<212> PRT
<213> Mus musculus

```

```

<220>
<221> SIGNAL
<222> (1)...(19)

```

```

<400> 14
Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
          -15                -10                -5
Ser Ser Ser Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val
    1          5          10
Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Ile
    15          20          25
Ile His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro
    30          35          40          45
Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
          50          55          60
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
          65          70          75
Leu Lys Ile Lys Lys Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys
          80          85          90
Phe Gln Gly Ser His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
    95                100                105
Glu Leu Glu
110

```

```

<210> 15
<211> 426
<212> DNA
<213> Mus musculus

```

```

<220>
<221> CDS
<222> (1)...(426)

```

```

<221> sig_peptide
<222> (1)...(57)

```

```

<400> 15
atg gac agg ctt act tcc tca ttc ctg ctg ctg att gtc cct gca tat 48
Met Asp Arg Leu Thr Ser Ser Phe Leu Leu Leu Ile Val Pro Ala Tyr
          -15                -10                -5

```

100100942-120501

gtc ctg tcc cag gct act ctg aaa gag tct ggc cct gga ata ttg cag 96
 Val Leu Ser Gln Ala Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
 1 5 10

tcc tcc cag acc ctc agt ctg act tgt tct ttc tct ggg ttt tca ctg 144
 Ser Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
 15 20 25

agc act tct ggt atg gga gtg agc tgg att cgt cag cct tca gga aag 192
 Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys
 30 35 40 45

ggt ctg gag tgg ctg gca cac att tac tgg gat gat gac aag cgc tat 240
 Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
 50 55 60

aac cca tcc ctg aag agc cgg ctc aca atc tcc aag gat acc tcc aga 288
 Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Arg
 65 70 75

aag cag gta ttc ctc aag atc acc agt gtg gac cct gca gat act gcc 336
 Lys Gln Val Phe Leu Lys Ile Thr Ser Val Asp Pro Ala Asp Thr Ala
 80 85 90

aca tac tac tgt gtt cga agg ccc att act ccg gta cta gtc gat gct 384
 Thr Tyr Tyr Cys Val Arg Arg Pro Ile Thr Pro Val Leu Val Asp Ala
 95 100 105

atg gac tac tgg ggt caa gga acc tca gtc acc gtc tcc tca 426
 Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
 110 115 120

<210> 16
 <211> 142
 <212> PRT
 <213> Mus musculus

<220>
 <221> SIGNAL
 <222> (1)...(19)

<400> 16
 Met Asp Arg Leu Thr Ser Ser Phe Leu Leu Leu Ile Val Pro Ala Tyr
 -15 -10 -5
 Val Leu Ser Gln Ala Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
 1 5 10
 Ser Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
 15 20 25
 Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys
 30 35 40 45
 Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
 50 55 60
 Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Arg
 65 70 75
 Lys Gln Val Phe Leu Lys Ile Thr Ser Val Asp Pro Ala Asp Thr Ala

10010942-120601

		80				85				90					
Thr	Tyr	Tyr	Cys	Val	Arg	Arg	Pro	Ile	Thr	Pro	Val	Leu	Val	Asp	Ala
	95					100					105				
Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser		
110					115					120					

```
<210> 17
<211> 136
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Primer

```
<400> 17
tccgcaagct  tgcgcgccacc  atggacatgc  gcggtgcccg  ccagctgctg  ggcttgcgtg  60
tgctgtgggt  gtccggctcc  tccggctacg  tggtgatgac  ccagtccccc  ctgtccctgc  120
ccgtgacccc  cggcgca
136
```

```
<210> 18
<211> 131
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Primer

```
<400> 18
ctgggggggac tggccgggct tctgcagcag ccagttcagg taggtcttgc cgtcggagtc 60
cagcagggac tgggaggact tgcaggagat ggaggcgggc tcgccggggg tcacgggcag 120
ggacaggggg g                                     131
```

```
<210> 19
<211> 146
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Primer

```
<400> 19
acctgaactg gctgctgcag aagcccggcc agtcccccca gcgctgatc tacctgggtgt 60
ccaagctgga ctccggcgctg cccgaccgct tctccggctc cggctccggc accgacttca 120
ccctgaagat ctcccgcgctg gaggcc                                     146
```

```
<210> 20
<211> 142
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Primer

<400> 20
aattctagga tccactcacg cttgatctcc accttggtgc cctggccgaa ggtgcggggg 60
aagtgggtgc cctgccagca gtagtacacg cccacgtcct cggcctccac gcgggagatc 120
ttcagggtga agtcggtgcc gg 142

<210> 21
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 21
ctgggggggac tggccg 16

<210> 22
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 22
acctgaactg gctgctgcag aa 22

<210> 23
<211> 138
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 23
acagaaagct tgccgccacc atggagtttg ggctgagctg gctttttctt gtggctattt 60
taaaagggtg ccagtgtgag gtgcagctgc tggagtccgg cggcggcctg gtgcagcccg 120
gcggctccct gcgcctgt 138

<210> 24
<211> 135
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 24
gccgccggag cggatggagg ccaccactc caggcccttg ccgggggcct ggcgcaccca 60
ggacatgccg tagttggaga aggtgaagcc ggaggcggcg caggacaggc gcagggagcc 120
gccgggctgc accag 135

<210> 25
<211> 142
<212> DNA
<213> Artificial Sequence

10010942-13001

<220>

<223> Primer

<400> 25

ctggagtggg tggcctccat ccgctccggc ggcgggcgca cctactactc cgacaacgtg 60
 aagggccgct tcaccatctc ccgcgacaac gccaaagaact ccctgtacct gcagatgaac 120
 tccctgcgcg ccgaggacac cg 142

<210> 26

<211> 144

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 26

ctgcaaggat ccaactaccg gaggacacgg tcaccagggt gccctggccc cagtagtcgg 60
 aggagccgga gtagtggtcg tagcgacgc agtagtacag ggcggtgtcc tcggcgcgca 120
 gggagttcat ctgcaggtac aggg 144

<210> 27

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 27

gccgccggag cggatg 16

<210> 28

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 28

ctggagtggg tggcctccat 20

<210> 29

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 29

tccgcaagct tgccgccac 19

T0502T-2460700T

<210> 30
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 30
aattctagga tccactcacg ctgatctc 29

<210> 31
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 31
acagaaagct tgccgccacc atg 23

<210> 32
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 32
ctgcaaggat ccactcacgc ga 22

<210> 33
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> internal peptide

<400> 33
Asp Ala Glu Phe Arg His Asp Ser Gly Tyr
1 5 10

<210> 34
<211> 402
<212> DNA
<213> Artificial Sequence

<220>
<223> h3D6 version 1 VL

<400> 34
 atggacatgc gcgtgcccgc ccagctgctg ggcttgcgtga tgctgtgggt gtccgggtcc 60
 tccggctacg tggatgatgac ccagtcctcc ctgtccctgc ccgtgacccc cggcgagccc 120
 gcctccatct cctgcaagtc ctcccagtc ctgtgtggact ccgacggcaa gacctacctg 180
 aactggctgc tgcagaagcc cggccagtc ccccagcgcc tgatctacct ggtgtccaag 240
 ctggactccg gcgtgcccga ccgtttctcc ggctccggct ccggcaccga cttcaccctg 300
 aagatctccc gcgtggaggc cgaggacgtg ggctgtgtact actgctggca gggcaccac 360
 ttccccgcga ccttcggcca gggcaccaag gtggagatca ag 402

<210> 35

<211> 402

<212> DNA

<213> Artificial Sequence

<220>

<223> h3D6 version 2 VL

<400> 35
 atggacatgc gcgtgcccgc ccagctgctg ggcttgcgtga tgctgtgggt gtccgggtcc 60
 tccggcgacg tggatgatgac ccagtcctcc ctgtccctgc ccgtgacccc cggcgagccc 120
 gcctccatct cctgcaagtc ctcccagtc ctgtgtggact ccgacggcaa gacctacctg 180
 aactggctgc tgcagaagcc cggccagtc ccccagcgcc tgatctacct ggtgtccaag 240
 ctggactccg gcgtgcccga ccgtttctcc ggctccggct ccggcaccga cttcaccctg 300
 aagatctccc gcgtggaggc cgaggacgtg ggctgtgtact actgctggca gggcaccac 360
 ttccccgcga ccttcggcca gggcaccaag gtggagatca ag 402

<210> 36

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<223> h3D6 version 1 VH

<400> 36
 atggagtttg ggctgagctg gctttttctt gtggctatatt taaaagggtg ccagtgtgag 60
 gtgcagctgc tggagtcccg cggcgccctg gtgcagcccg gcggctccct gcgcctgtcc 120
 tgcgcgcct cgggcttcac cttctccaac tacggcatgt cctgggtgcg ccaggcccc 180
 ggcaagggcc tggagtgggt ggctccatc cgtccggcg gcggccgcac ctactactcc 240
 gacaacgtga agggccgctt caccatctcc cgcgacaacg ccaagaactc cctgtacctg 300
 cagatgaact ccctgcgcgc cgaggacacc gccctgtact actgcgtgcg ctacgaccac 360
 tactccggct cctccgacta ctggggccag ggcaccctgg tgaccgtgtc ctcc 414

<210> 37

<211> 414

<212> DNA

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 tgcgcgcct cgggcttcac cttctccaac tacggcatgt cctgggtgcg ccaggcccc 180
 ggcaagggcc tggagtgggt ggctccatc cgtccggcg gcggccgcac ctactactcc 240
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<212> PRT

<213> Homo Sapiens

<400> 38

Met	Leu	Pro	Gly	Leu	Ala	Leu	Leu	Leu	Leu	Ala	Ala	Trp	Thr	Ala	Arg	1	5	10	15
Ala	Leu	Glu	Val	Pro	Thr	Asp	Gly	Asn	Ala	Gly	Leu	Leu	Ala	Glu	Pro	20	25	30	
Gln	Ile	Ala	Met	Phe	Cys	Gly	Arg	Leu	Asn	Met	His	Met	Asn	Val	Gln	35	40	45	
Asn	Gly	Lys	Trp	Asp	Ser	Asp	Pro	Ser	Gly	Thr	Lys	Thr	Cys	Ile	Asp	50	55	60	
Thr	Lys	Glu	Gly	Ile	Leu	Gln	Tyr	Cys	Gln	Glu	Val	Tyr	Pro	Glu	Leu	65	70	75	80
Gln	Ile	Thr	Asn	Val	Glu	Ala	Asn	Gln	Pro	Val	Thr	Ile	Gln	Asn		85	90	95	
Trp	Cys	Lys	Arg	Gly	Arg	Lys	Gln	Cys	Lys	Thr	His	Pro	His	Phe	Val	100	105	110	
Ile	Pro	Tyr	Arg	Cys	Leu	Val	Gly	Glu	Phe	Val	Ser	Asp	Ala	Leu	Leu	115	120	125	
Val	Pro	Asp	Lys	Cys	Lys	Phe	Leu	His	Gln	Glu	Arg	Met	Asp	Val	Cys	130	135	140	
Glu	Thr	His	Leu	His	Trp	His	Thr	Val	Ala	Lys	Glu	Thr	Cys	Ser	Glu	145	150	155	160
Lys	Ser	Thr	Asn	Leu	His	Asp	Tyr	Gly	Met	Leu	Leu	Pro	Cys	Gly	Ile	165	170	175	
Asp	Lys	Phe	Arg	Gly	Val	Glu	Phe	Val	Cys	Cys	Pro	Leu	Ala	Glu	Glu	180	185	190	
Ser	Asp	Asn	Val	Asp	Ser	Ala	Asp	Ala	Glu	Glu	Asp	Asp	Ser	Asp	Val	195	200	205	
Trp	Trp	Gly	Gly	Ala	Asp	Thr	Asp	Tyr	Ala	Asp	Gly	Ser	Glu	Asp	Lys	210	215	220	
Val	Val	Glu	Val	Ala	Glu	Glu	Glu	Glu	Val	Ala	Glu	Val	Glu	Glu	Glu	225	230	235	240
Glu	Ala	Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gly	Asp	Glu	Val	Glu	Glu	245	250	255	
Glu	Ala	Glu	Glu	Pro	Tyr	Glu	Glu	Ala	Thr	Glu	Arg	Thr	Thr	Ser	Ile	260	265	270	
Ala	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Glu	Ser	Val	Glu	Glu	Val	Val	Arg	275	280	285	
Glu	Val	Cys	Ser	Glu	Gln	Ala	Glu	Thr	Gly	Pro	Cys	Arg	Ala	Met	Ile	290	295	300	
Ser	Arg	Trp	Tyr	Phe	Asp	Val	Thr	Glu	Gly	Lys	Cys	Ala	Pro	Phe	Phe	305	310	315	320
Tyr	Gly	Gly	Cys	Gly	Gly	Asn	Arg	Asn	Asn	Phe	Asp	Thr	Glu	Glu	Tyr	325	330	335	
Cys	Met	Ala	Val	Cys	Gly	Ser	Ala	Met	Ser	Gln	Ser	Leu	Leu	Lys	Thr	340	345	350	
Thr	Gln	Glu	Pro	Leu	Ala	Arg	Asp	Pro	Val	Lys	Leu	Pro	Thr	Thr	Ala	355	360	365	
Ala	Ser	Thr	Pro	Asp	Ala	Val	Asp	Lys	Tyr	Leu	Glu	Thr	Pro	Gly	Asp	370	375	380	

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Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala
 385 390 395 400
 Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala
 405 410 415
 Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile
 420 425 430
 Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn
 435 440 445
 Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met
 450 455 460
 Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu
 465 470 475 480
 Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys
 485 490 495
 Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe
 500 505 510
 Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser
 515 520 525
 Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser
 530 535 540
 Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp
 545 550 555 560
 Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val
 565 570 575
 Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala
 580 585 590
 Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro
 595 600 605
 Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe
 610 615 620
 Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val
 625 630 635 640
 Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser
 645 650 655
 Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp
 660 665 670
 Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu
 675 680 685
 Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly
 690 695 700
 Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
 705 710 715 720
 Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
 725 730 735
 Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
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14

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